SEQUENCE LISTING

<110> Wilkins, Thea A.
The Regents of the University of California

<120> Cotton Transcription Factors and Their Uses

<130> 023070-095600US

<140> US 09/453,387
<141> 1999-12-02

<160> 26

<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
<213> Gossypium hirsutum

<220>
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<222> (59)..(943)
<223> GhMYB1

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Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
1 5 10 15

tgg acc aaa gag gaa gat caa cgc ctc atc aac tac atc cgt gtc cat 154
Trp Thr Lys Glu Glu Asp Gln Arg Leu Ile Asn Tyr Ile Arg Val His
20 25 30

ggt gaa ggc tgc tgg cgt tcc ctc ccc aaa gct gct ggg ctg ctt aga 202
Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35 40 45

tgt ggt aag agt tgc aga tta aga tgg ata aac tac ttg agg cct gat 250
Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

ctt aag aga gga aat ttc act gaa gaa gaa gat gag ctt atc atc aag 298
Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
65 70 75 80

ctt cac agt tta ctt gga aac aaa tgg tca ttg att gct gga aga tta 346
Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85 90 95

cca gga aga aca gat aat gag ata aag aac tac tgg aac aca cac atc 394
Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

aaa aga aag ctt ata agc aga gga att gat cca caa act cat cgt cct 442
Lys Arg Lys Leu Ile Ser Arg Gly Ile Asp Pro Gln Thr His Arg Pro
115 120 125

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ctc aat caa acg gcc aat acc aac aca gtc aca gcc ccc acc gaa ttg   490
Leu Asn Gln Thr Ala Asn Thr Asn Thr Val Thr Ala Pro Thr Glu Leu
    130                 135                 140

gat ttc aga aac tcg ccc aca tcc gtt tcc aaa tcc agt tcc atc aaa   538
Asp Phe Arg Asn Ser Pro Thr Ser Val Ser Lys Ser Ser Ser Ile Lys
145                 150                 155                 160

aac ccg tct ctg gat ttc aat tac aat gaa ttt caa ttc aag tcc aac   586
Asn Pro Ser Leu Asp Phe Asn Tyr Asn Glu Phe Gln Phe Lys Ser Asn
                165                 170                 175

aca gat tcc ctt gaa gaa ccc aac tgt aca gcc agc agt ggc atg act   634
Thr Asp Ser Leu Glu Glu Pro Asn Cys Thr Ala Ser Ser Gly Met Thr
            180                 185                 190

aca gat gaa gag caa caa gaa cag ctg cac aag aag cag caa tac ggt   682
Thr Asp Glu Glu Gln Gln Glu Gln Leu His Lys Lys Gln Gln Tyr Gly
        195                 200                 205

ccg agc aat ggg caa gac ata aat ttg gag ctg tcg att ggg att gtt   730
Pro Ser Asn Gly Gln Asp Ile Asn Leu Glu Leu Ser Ile Gly Ile Val
    210                 215                 220

tca gct gac tca tct cgg gta tca aat gcc aac tcg gcc gag tcg aaa   778
Ser Ala Asp Ser Ser Arg Val Ser Asn Ala Asn Ser Ala Glu Ser Lys
225                 230                 235                 240

cca aag gta gat aac aac aat ttc cag ttt ctt gaa caa gct atg gtg   826
Pro Lys Val Asp Asn Asn Asn Phe Gln Phe Leu Glu Gln Ala Met Val
                245                 250                 255

gct aag gcg gta tgt ttg tgt tgg caa tta ggt ttt gga aca agt gaa   874
Ala Lys Ala Val Cys Leu Cys Trp Gln Leu Gly Phe Gly Thr Ser Glu
            260                 265                 270

att tgt agg aac tgt caa aat tca aat tca aat ggc ttc tat agt tat   922
Ile Cys Arg Asn Cys Gln Asn Ser Asn Ser Asn Gly Phe Tyr Ser Tyr
        275                 280                 285

tgt aga ccc ttg gat tca tag ggtcatcttt ttcttctttc tttctgtttt      973
Cys Arg Pro Leu Asp Ser
    290                 295

taggagataa attaatgctt aattattaaa aaa                              1006


<210> 2
<211> 294
<212> PRT
<213> Gossypium hirsutum

<400> 2
Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
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Trp Thr Lys Glu Glu Asp Gln Arg Leu Ile Asn Tyr Ile Arg Val His
             20                  25                  30
Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
         35                  40                  45
Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
     50                  55                  60
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Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
 65                  70                  75                  80
Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
                85                  90                  95
Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
            100                 105                 110
Lys Arg Lys Leu Ile Ser Arg Gly Ile Asp Pro Gln Thr His Arg Pro
        115                 120                 125
Leu Asn Gln Thr Ala Asn Thr Asn Thr Val Thr Ala Pro Thr Glu Leu
    130                 135                 140
Asp Phe Arg Asn Ser Pro Thr Ser Val Ser Lys Ser Ser Ser Ile Lys
145                 150                 155                 160
Asn Pro Ser Leu Asp Phe Asn Tyr Asn Glu Phe Gln Phe Lys Ser Asn
                165                 170                 175
Thr Asp Ser Leu Glu Glu Pro Asn Cys Thr Ala Ser Ser Gly Met Thr
            180                 185                 190
Thr Asp Glu Glu Gln Gln Glu Gln Leu His Lys Lys Gln Gln Tyr Gly
        195                 200                 205
Pro Ser Asn Gly Gln Asp Ile Asn Leu Glu Leu Ser Ile Gly Ile Val
    210                 215                 220
Ser Ala Asp Ser Ser Arg Val Ser Asn Ala Asn Ser Ala Glu Ser Lys
225                 230                 235                 240
Pro Lys Val Asp Asn Asn Asn Phe Gln Phe Leu Glu Gln Ala Met Val
                245                 250                 255
Ala Lys Ala Val Cys Leu Cys Trp Gln Leu Gly Phe Gly Thr Ser Glu
            260                 265                 270
Ile Cys Arg Asn Cys Gln Asn Ser Asn Ser Asn Gly Phe Tyr Ser Tyr
        275                 280                 285
Cys Arg Pro Leu Asp Ser
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<210> 3
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<212> DNA
<213> Gossypium hirsutum

<220>
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<222> (72)..(752)
<223> GhMYB6

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             Met Arg Lys Pro Cys Cys Asp Lys Gln Gly Thr Asn Lys
               1               5                  10

gga gcc tgg tcc aag caa gaa gat caa aag ctc att gat tat ata cgt   158
Gly Ala Trp Ser Lys Gln Glu Asp Gln Lys Leu Ile Asp Tyr Ile Arg
     15                  20                  25

att cat ggt gaa ggc tgt tgg cgt tcc ctc ccc aaa gct gca ggt ttg   206
Ile His Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu
 30                  35                  40                  45

cac cgt tgc ggt aaa agt tgc agg ctg aga tgg ata aat tac tta aga   254
His Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg
                50                  55                  60
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cca gat atc aaa cgt ggt aac ttt gct caa gac gaa gag gac tta att   302
Pro Asp Ile Lys Arg Gly Asn Phe Ala Gln Asp Glu Glu Asp Leu Ile
            65                  70                  75

atc aaa ctc cat gct ctc ctt ggt aac cgg tgg tca ctg ata gct ggt   350
Ile Lys Leu His Ala Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly
        80                  85                  90

aga tta cca gga aga aca gat aat gaa gtg aag aac tat tgg aat tcc   398
Arg Leu Pro Gly Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser
    95                  100                 105

cat ata aag aga aag cta atg aag atg ggg atc gat cct aat aac cat   446
His Ile Lys Arg Lys Leu Met Lys Met Gly Ile Asp Pro Asn Asn His
110                 115                 120                 125

aag ttg aac caa tat cct cat cat gtt ggt ccc ctt aac ccc acc acc   494
Lys Leu Asn Gln Tyr Pro His His Val Gly Pro Leu Asn Pro Thr Thr
                130                 135                 140

acc aac tcc atg gat gtg gca tgt aag ctt aga gtg tgt tca aca gac   542
Thr Asn Ser Met Asp Val Ala Cys Lys Leu Arg Val Cys Ser Thr Asp
            145                 150                 155

aat gat gat ggg atc tca gat gct gca agt tat ctc gaa gac gca aca   590
Asn Asp Asp Gly Ile Ser Asp Ala Ala Ser Tyr Leu Glu Asp Ala Thr
        160                 165                 170

ccg ccc act ggt ata tcc aac ttg gac ctt gat ctc aca att gct ttt   638
Pro Pro Thr Gly Ile Ser Asn Leu Asp Leu Asp Leu Thr Ile Ala Phe
    175                 180                 185

cct tcg agt cct atc aag aat att att gaa gaa agc cag cag aaa aca   686
Pro Ser Ser Pro Ile Lys Asn Ile Ile Glu Glu Ser Gln Gln Lys Thr
190                 195                 200                 205

gca tct att gta aca aat gat gaa gaa gaa caa tat aca gtc cct acc   734
Ala Ser Ile Val Thr Asn Asp Glu Glu Glu Gln Tyr Thr Val Pro Thr
                210                 215                 220

ctt ctt ctt ttc aga tga gacaaaaaaa aaagcctcac acatgtggag          782
Leu Leu Leu Phe Arg
            225

attcgtgcaa aagacctaaa ggcttacgaa ggcaacatgc acgccattgt caaattcttt 842

tggatgatgg attgaaacca tatccttgtc cattagaaag gaggaagata agctaaaact 902

gtattattgt gtataaattt ggtagaaaga aagatttcaa cttaagaatt aggatcaaat 962

aactgaatga atgaacgaat tgcagataag ttgttaggag gttttcaatc aacttatctg 1022

caattaattt ggtggagctg atgtaggatg atgagttcat cgtacatgaa ctgaaccttt 1082

gatatttcag gctctaattg tctgtttgta tgcgtaaaga tattcttcaa tgtgagatca 1142

gctaaaaaa                                                        1151
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<210> 4
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<212> PRT
<213> Gossypium hirsutum

<400> 4
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Ser Lys Gln Glu Asp Gln Lys Leu Ile Asp Tyr Ile Arg Ile His Gly
20 25 30
Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu His Arg Cys
35 40 45
Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Ile
50 55 60
Lys Arg Gly Asn Phe Ala Gln Asp Glu Glu Asp Leu Ile Ile Lys Leu
65 70 75 80
His Ala Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro
85 90 95
Gly Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser His Ile Lys
100 105 110
Arg Lys Leu Met Lys Met Gly Ile Asp Pro Asn Asn His Lys Leu Asn
115 120 125
Gln Tyr Pro His His Val Gly Pro Leu Asn Pro Thr Thr Thr Asn Ser
130 135 140
Met Asp Val Ala Cys Lys Leu Arg Val Cys Ser Thr Asp Asn Asp Asp
145 150 155 160
Gly Ile Ser Asp Ala Ala Ser Tyr Leu Glu Asp Ala Thr Pro Pro Thr
165 170 175
Gly Ile Ser Asn Leu Asp Leu Asp Leu Thr Ile Ala Phe Pro Ser Ser
180 185 190
Pro Ile Lys Asn Ile Ile Glu Glu Ser Gln Gln Lys Thr Ala Ser Ile
195 200 205
Val Thr Asn Asp Glu Glu Glu Gln Tyr Thr Val Pro Thr Leu Leu Leu
210 215 220
Phe Arg
225

<210> 5
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<212> DNA
<213> Gossypium hirsutum

<220>
<221> CDS
<222> (86)..(994)
<223> GhMYB7

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Met Gly Arg Ser Pro Cys Cys Ser Lys
1 5

gaa ggc ctt aac aga gga gct tgg act gct ctt gaa gac aaa att ctt 160
Glu Gly Leu Asn Arg Gly Ala Trp Thr Ala Leu Glu Asp Lys Ile Leu
10 15 20 25

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aaa gat tat atc aaa gta cac ggt gaa ggt cgt tgg aga aat ctc ccc   208
Lys Asp Tyr Ile Lys Val His Gly Glu Gly Arg Trp Arg Asn Leu Pro
                 30                  35                  40

aaa aga gct ggt ctt aag aga tgt ggg aaa agt tgt agg ctt cgg tgg   256
Lys Arg Ala Gly Leu Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp
             45                  50                  55

ttg aat tat ttg aga cct gat att aaa aga ggt aac ata tca cct gac   304
Leu Asn Tyr Leu Arg Pro Asp Ile Lys Arg Gly Asn Ile Ser Pro Asp
         60                  65                  70

gag gaa gag ctt atc atc aaa ctc cac aaa ctc ttg gga aac aga tgg   352
Glu Glu Glu Leu Ile Ile Lys Leu His Lys Leu Leu Gly Asn Arg Trp
     75                  80                  85

tct ttg ata gct ggg agg ctt cca gga cga aca gac aat gaa ata aag   400
Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys
 90                  95                 100                 105

aat tac tgg aac acc aac tta agt aaa aga gtt tcc gat cgt caa aag   448
Asn Tyr Trp Asn Thr Asn Leu Ser Lys Arg Val Ser Asp Arg Gln Lys
                110                 115                 120

tca ccc gcc gct cct tcg aaa aat ccc gag gcg gct cga cga gga act   496
Ser Pro Ala Ala Pro Ser Lys Asn Pro Glu Ala Ala Arg Arg Gly Thr
            125                 130                 135

gct ggt aat ggc aat acc aat ggt aat ggt agt ggt agt tcc tcg aca   544
Ala Gly Asn Gly Asn Thr Asn Gly Asn Gly Ser Gly Ser Ser Ser Thr
        140                 145                 150

cac gtg gtg cgg aca agg gcg aca agg tgc tcc aag gtt ttc ata aac   592
His Val Val Arg Thr Arg Ala Thr Arg Cys Ser Lys Val Phe Ile Asn
    155                 160                 165

cct cct cac tac aca caa aac aga gac cca aag cct tct tca act tgt   640
Pro Pro His Tyr Thr Gln Asn Arg Asp Pro Lys Pro Ser Ser Thr Cys
170                 175                 180                 185

tca aat cat ggg gat cac cgg gaa cct aaa aca atg aat gag ttg tta   688
Ser Asn His Gly Asp His Arg Glu Pro Lys Thr Met Asn Glu Leu Leu
                190                 195                 200

tta ccg ata atg tca gaa tcc gag aat gaa ggg acg acc gat cat ata   736
Leu Pro Ile Met Ser Glu Ser Glu Asn Glu Gly Thr Thr Asp His Ile
            205                 210                 215

tca tcg gat ttt aca ttt gac ttc aac atg gga gag ttt tgt tta tcg   784
Ser Ser Asp Phe Thr Phe Asp Phe Asn Met Gly Glu Phe Cys Leu Ser
        220                 225                 230

gat ctt ttg aat tcc gat ttc tgc gat gta aac gag ctt aat tac agc   832
Asp Leu Leu Asn Ser Asp Phe Cys Asp Val Asn Glu Leu Asn Tyr Ser
    235                 240                 245

aat ggt ttt gat tcg tca ccc tca ccg gat cag cct cct atg gat ttc   880
Asn Gly Phe Asp Ser Ser Pro Ser Pro Asp Gln Pro Pro Met Asp Phe
250                 255                 260                 265
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tcc gac gaa atg cta aaa gag tgg acg gcc gcc gcc tcc act cac tgc   928
Ser Asp Glu Met Leu Lys Glu Trp Thr Ala Ala Ala Ser Thr His Cys
                270                 275                 280

tgt cac caa agt gcg gct tcc aat ctc cag tcc ttg cct cca ttt att   976
Cys His Gln Ser Ala Ala Ser Asn Leu Gln Ser Leu Pro Pro Phe Ile
            285                 290                 295

gaa aat gga att gaa tga ccttgaaaaa ataaaagacg aaaaatattt          1024
Glu Asn Gly Ile Glu
        300

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<210> 6
<211> 302
<212> PRT
<213> Gossypium hirsutum

<400> 6
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             20                  25                  30
Gly Glu Gly Arg Trp Arg Asn Leu Pro Lys Arg Ala Gly Leu Lys Arg
         35                  40                  45
Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp
     50                  55                  60
Ile Lys Arg Gly Asn Ile Ser Pro Asp Glu Glu Glu Leu Ile Ile Lys
 65                  70                  75                  80
Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu
                 85                  90                  95
Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr Asn Leu
            100                 105                 110
Ser Lys Arg Val Ser Asp Arg Gln Lys Ser Pro Ala Ala Pro Ser Lys
        115                 120                 125
Asn Pro Glu Ala Ala Arg Arg Gly Thr Ala Gly Asn Gly Asn Thr Asn
    130                 135                 140
Gly Asn Gly Ser Gly Ser Ser Ser Thr His Val Val Arg Thr Arg Ala
145                 150                 155                 160
Thr Arg Cys Ser Lys Val Phe Ile Asn Pro Pro His Tyr Thr Gln Asn
                165                 170                 175
Arg Asp Pro Lys Pro Ser Ser Thr Cys Ser Asn His Gly Asp His Arg
            180                 185                 190
Glu Pro Lys Thr Met Asn Glu Leu Leu Leu Pro Ile Met Ser Glu Ser
        195                 200                 205
Glu Asn Glu Gly Thr Thr Asp His Ile Ser Ser Asp Phe Thr Phe Asp
    210                 215                 220
Phe Asn Met Gly Glu Phe Cys Leu Ser Asp Leu Leu Asn Ser Asp Phe
225                 230                 235                 240
Cys Asp Val Asn Glu Leu Asn Tyr Ser Asn Gly Phe Asp Ser Ser Pro
                245                 250                 255
Ser Pro Asp Gln Pro Pro Met Asp Phe Ser Asp Glu Met Leu Lys Glu
            260                 265                 270
Trp Thr Ala Ala Ala Ser Thr His Cys Cys His Gln Ser Ala Ala Ser
        275                 280                 285
Asn Leu Gln Ser Leu Pro Pro Phe Ile Glu Asn Gly Ile Glu
    290                 295                 300
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<210> 7
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<223> GhMYB8

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<223> n = g, a, c or t

<220>
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<222> (22)
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cggcacgaga ctccaacaa atg tcc atg aaa aaa gaa ggt gaa att cta tac 112
Met Ser Met Lys Lys Glu Gly Glu Ile Leu Tyr
1 5 10

aaa aag gga tta tgg gca atg gag gaa gac aag tta ctc att gat tat 160
Lys Lys Gly Leu Trp Ala Met Glu Glu Asp Lys Leu Leu Ile Asp Tyr
15 20 25

gtc aat gtc cat gga aaa gga caa tgg aac aaa ata gcc aac aga aca 208
Val Asn Val His Gly Lys Gly Gln Trp Asn Lys Ile Ala Asn Arg Thr
30 35 40

ggt ttg aag aga agt ggg aaa agt tgt cgg cta agg tgg atg aat tac 256
Gly Leu Lys Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr
45 50 55

ctg agt cct aac gtt aaa aag ggt gat ttt tct gaa gaa gaa gaa gac 304
Leu Ser Pro Asn Val Lys Lys Gly Asp Phe Ser Glu Glu Glu Glu Asp
60 65 70 75

ctc gtc att aga ctt cat aag ctt ctt gga aac agg tgg tct ttg att 352
Leu Val Ile Arg Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile
80 85 90

gcg aaa cga gtt cca ggt cga act gac aat caa gtc aag aat tac tgg 400
Ala Lys Arg Val Pro Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp
95 100 105

aat agt cat ttg agg aag aaa cta ggg atc att gat caa aac aag aca 448
Asn Ser His Leu Arg Lys Lys Leu Gly Ile Ile Asp Gln Asn Lys Thr
110 115 120

agg atc gat ttt tgt caa agt tca aag caa gtc aaa gtg tgt cat gtt 496
Arg Ile Asp Phe Cys Gln Ser Ser Lys Gln Val Lys Val Cys His Val
125 130 135

```
gat gag gca gcc acg gat cca agt cct gga cat gga aca acc act gaa   544
Asp Glu Ala Ala Thr Asp Pro Ser Pro Gly His Gly Thr Thr Thr Glu
140                 145                 150                 155

acc acg ggt ata aca gtg gat cag agt aac cag cag gaa gtc att gat   592
Thr Thr Gly Ile Thr Val Asp Gln Ser Asn Gln Gln Glu Val Ile Asp
                160                 165                 170

cat cgg gtc tta aac aat act act caa gaa tca atg acc agt gag agt   640
His Arg Val Leu Asn Asn Thr Thr Gln Glu Ser Met Thr Ser Glu Ser
            175                 180                 185

tat atc aac act ttc tgg att cct gac cat gat tat gag cta agt aca   688
Tyr Ile Asn Thr Phe Trp Ile Pro Asp His Asp Tyr Glu Leu Ser Thr
        190                 195                 200

ctt gcc atg att gac cat gat tat gag cta agt aca ctt gcc atg att   736
Leu Ala Met Ile Asp His Asp Tyr Glu Leu Ser Thr Leu Ala Met Ile
    205                 210                 215

gac cac ttc cat gaa tgt tct tct ttt cat ctt agc tag agactatgtt    785
Asp His Phe His Glu Cys Ser Ser Phe His Leu Ser
220                 225                 230

attagattcg ggttttattt ttagatataa gtatgcatct aacatggcaa tgttaaattt 845

ttcaaaagat ttttcatgta tttgagcagt tcatgtgttt gaagattaag atatttctga 905

aaaaaaaaaa aaaaaaaaac cgaggggggc ccggtaccc                         944
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<210> 8
<211> 231
<212> PRT
<213> Gossypium hirsutum

<400> 8

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Met Ser Met Lys Lys Glu Gly Glu Ile Leu Tyr Lys Lys Gly Leu Trp
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Ala Met Glu Glu Asp Lys Leu Leu Ile Asp Tyr Val Asn Val His Gly
            20                  25                  30
Lys Gly Gln Trp Asn Lys Ile Ala Asn Arg Thr Gly Leu Lys Arg Ser
        35                  40                  45
Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Ser Pro Asn Val
    50                  55                  60
Lys Lys Gly Asp Phe Ser Glu Glu Glu Glu Asp Leu Val Ile Arg Leu
65                  70                  75                  80
His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Lys Arg Val Pro
                85                  90                  95
Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp Asn Ser His Leu Arg
            100                 105                 110
Lys Lys Leu Gly Ile Ile Asp Gln Asn Lys Thr Arg Ile Asp Phe Cys
        115                 120                 125
Gln Ser Ser Lys Gln Val Lys Val Cys His Val Asp Glu Ala Ala Thr
    130                 135                 140
Asp Pro Ser Pro Gly His Gly Thr Thr Thr Glu Thr Thr Gly Ile Thr
145                 150                 155                 160
Val Asp Gln Ser Asn Gln Gln Glu Val Ile Asp His Arg Val Leu Asn
                165                 170                 175
Asn Thr Thr Gln Glu Ser Met Thr Ser Glu Ser Tyr Ile Asn Thr Phe
            180                 185                 190
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Trp Ile Pro Asp His Asp Tyr Glu Leu Ser Thr Leu Ala Met Ile Asp
195 200 205
His Asp Tyr Glu Leu Ser Thr Leu Ala Met Ile Asp His Phe His Glu
210 215 220
Cys Ser Ser Phe His Leu Ser
225 230

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate 'universal' MYB primer

<220>
<221> modified_base
<222> (3)
<223> n = g, a, c or t

<220>
<221> modified_base
<222> (15)
<223> n = i

<400> 9
ggnaaragyt gymgnttrag 20

<210> 10
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate 'universal' MYB primer

<220>
<221> modified_base
<222> (17)
<223> n = g, a, c or t

<400> 10
srttrtctgt tckkccngg 19

<210> 11
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:highly conserved peptide coded by degenerate 'universal' MYB primer

<400> 11
Gly Lys Ser Cys Arg Leu
1 5

<210> 12
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:highly conserved peptide coded by degenerate 'universal' MYB primer

<400> 12
Pro Gly Arg Thr Asp Asn
1 5

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide primer COT105

<400> 13
aagcagagga attgatccac 20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide primer COT106

<400> 14
accctatgaa tccaagggtc 20

<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide primer COT107

<400> 15
cctcggaaca aattgtgcc 19

<210> 16
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide primer COT108

<400> 16
cctcggaaca aattgtgcc 19

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide primer COT109

<400> 17
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<210> 18
<211> 20
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<220>
<223> Description of Artificial Sequence:oligonucleotide primer COT110

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<210> 19
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<210> 20
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<223> Description of Artificial Sequence:oligonucleotide primer COT112

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<210> 21
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<210> 22
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<223> Description of Artificial Sequence:oligonucleotide primer COT114

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<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide primer COT115

<400> 23
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<210> 24
<211> 20
<212> DNA
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<223> Description of Artificial Sequence:oligonucleotide primer COT116

<400> 24
acaatggcgt gcatgttgcc 20

<210> 25
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:conserved motif
within the basic 'transregulatory region 1' (TRR1)
domain

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<223> Xaa = any amino acid

<400> 25
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1 5

<210> 26
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:cysteine-rich
zinc-finger motif

<220>
<221> MOD_RES
<222> (2)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
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<223> Xaa = any amino acid

B1 cont

<220>
<221> MOD_RES
<222> (15)..(16)
<223> Xaa = any amino acid

<400> 26
Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
1 5 10 15
Cys